

5'	9	18	27	36	45	54
GG GGA AGC AGC	TGG AGT	GCG ACC	GCC ACC	GCA GCC	CTG CAA	CCG CCA
						GTC
GGA GGT GCA GTC	CGT AGG	CCC CCC	TGG CCC	CCG GGT	GGG CCC	AGT CGG
						CGC
CGC TCC CGA GGA	GCT GCA	AGG AGG	CTC GCC	CCT GCC	GGA GGG	CGC GGG
						GTC
CGC GGA GAA AGT	GAA GAG	AGG AGG	AAA TTG	GAA AAT	TGT GAG	TTC TGA
						TAC
TGC TCC TCC TTG	CGT GGA	AAA GGA	GAA GAA	ACT GCA	TGC ATA	TTC AGC
						GTC
CTA TAT TCA AAG	GAT ATT	CTT CTT	GAT GAT	GGA AGT	GTC CGT	ATG GAA
						TCA
ATC TCT ATG ATG	GGA AGC	CCT CCT	AAG AGC	CTT AGT	GAA ACT	TGT CCT
						AAT GGC
I S M M G S	M G S P K S L S E T C L P N G					

FIGURE 1A

FIGURE 1B

387	ATA	AAT	GGT	ATC	AAA	GAT	GCA	AGG	AAG	GTC	ACT	GTA	GGT	GTG	ATT	GGA	AGT	GGA	432
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	I	N	G	I	K	D	A	R	K	V	T	V	G	V	I	G	S	G	
441	GAT	TTT	GCC	AAA	TCC	TTG	ACC	ATT	CGA	CTT	ATT	AGA	TGC	GGC	TAT	CAT	GTG	GTC	486
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	D	F	A	K	S	L	T	I	R	L	I	R	C	G	Y	H	V	V	
495	ATA	GGA	AGT	AGA	AAT	CCT	AAG	TTT	GCT	TCT	GAA	TTT	TTT	CCT	CAT	GTG	GTA	GAT	540
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	I	G	S	R	N	P	K	F	A	S	E	F	F	P	H	V	V	D	
549	GTC	ACT	CAT	CAT	GAA	GAT	GCT	CTC	ACA	AAA	ACA	AAT	ATA	ATA	TTT	GTT	GCT	ATA	594
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	V	T	H	H	E	D	A	L	T	K	T	N	I	I	F	V	A	I	
603	CAC	AGA	GAA	CAT	TAT	ACC	TCC	CTG	TGG	GAC	CTG	AGA	CAT	CTG	CTT	GTG	GGT	AAA	648
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	H	R	E	H	Y	T	S	L	W	D	L	R	H	L	L	V	G	K	

FIGURE 1B

657	ATC	CTG	ATT	GAT	GTG	AGC	AAT	AAC	ATG	AGG	ATA	AAC	CAG	TAC	CCA	GAA	TCC	AAT
	I	L	I	D	V	S	N	N	M	R	I	N	Q	Y	P	E	S	N
711	GCT	GAA	TAT	TTG	GCT	TCA	TTA	TTC	CCA	GAT	TCT	TTG	ATT	GTC	AAA	GGA	TTT	AAT
	A	E	Y	L	A	S	L	F	P	D	S	L	I	V	K	G	F	N
765	GTT	GTC	TCA	GCT	TGG	GCA	CTT	CAG	TTA	GGA	CCT	AAG	GAT	GCC	AGC	CGG	CAG	GTT
	V	V	S	A	A	W	A	L	Q	L	G	P	K	D	A	S	R	Q
819	TAT	ATA	TGC	AGC	AAC	AAT	ATT	CAA	GCG	CGA	CAA	CAG	GTT	ATT	GAA	CTT	GCC	CGC
	Y	I	C	S	N	N	I	Q	A	R	Q	Q	V	I	E	L	A	R
873	CAG	TTG	AAT	TTC	ATT	CCC	ATT	GAC	TTG	GGA	TCC	TTA	TCA	TCA	GCC	AGA	GAG	ATT
	Q	L	N	F	I	P	I	D	L	G	S	L	S	S	A	R	E	I

FIGURE 1C

Sequence Alignment

927	936	945	954	963	972
GAA AAT TTA CCC CTA CGA CTC TTT ACT CTC TGG AGA GGG CCA GTG GTG GTA GCT					
---	---	---	---	---	---
E N L P L R L L F T L W R G P V V A					
981	990	999	1008	1017	1026
ATA AGC TTG GCC ACA TTT TTT TTC CTT TAT TCC TTT GTC AGA GAT GTG ATT CAT					
---	---	---	---	---	---
I S L A T F F F L Y S F V R D V I H					
1035	1044	1053	1062	1071	1080
CCA TAT GCT AGA AAC CAA CAG AGT GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG					
---	---	---	---	---	---
P Y A R N Q Q S D F Y K I P I E I V					
1089	1098	1107	1116	1125	1134
AAT AAA ACC TTA CCT ATA GTT GCC ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA					
---	---	---	---	---	---
N K T L P I V A I T L L S L V Y L A					
1143	1152	1161	1170	1179	1188
GGT CTT CTG GCA GCT GCT TAT CAA CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT					
---	---	---	---	---	---
G L L A A A Y Q L Y Y G T K Y R R F					

FIGURE 1D

1197	1206	1215	1224	1233	1242
CCA CCT TGG TTG GAA ACC TGG TTA CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT					
---	---	---	---	---	---
P P W L E T W L Q C R K Q L G L L S					
1251	1260	1269	1278	1287	1296
TTT TTC TTC GCT ATG GTC CAT GTT GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG					
---	---	---	---	---	---
F F F A M V H V A Y S L C L P M R R					
1305	1314	1323	1332	1341	1350
TCA GAG AGA TAT TTG TTT CTC AAC ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT					
---	---	---	---	---	---
S E R Y L F L N M A Y Q Q V H A N I					
1359	1368	1377	1386	1395	1404
GAA AAC TCT TGG AAT GAG GAA GAA GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT					
---	---	---	---	---	---
E N S W N E E E V W R I E M Y I S F					
1413	1422	1431	1440	1449	1458
GGC ATA ATG AGC CTT GGC TTA CTT TCC CTC CTC CTG GCA GTC ACT TCT ATC CCT TCA					
---	---	---	---	---	---
G I M S L G L L S L L A V T S I P S					

FIGURE 1E

Figure 1F

1467	1476	1485	1494	1503	1512
GTG AGC AAT GCT TTA AAC TGG AGA GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA					
---	---	---	---	---	---
V S N A L N W R E F S F I Q S T L G					
1521	1530	1539	1548	1557	1566
TAT GTC GCT CTG CTC ATA AGT ACT TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA					
---	---	---	---	---	---
Y V A L L I S T F H V L I Y G W K R					
1575	1584	1593	1602	1611	1620
GCT TTT GAG GAA GAG TAC TAC AGA TTT TAT ACA CCA CCA AAC TTT GTT CTT GCT					
---	---	---	---	---	---
A F E E E Y Y R F Y T P P N F V L A					
1629	1638	1647	1656	1665	1674
CTT GTT TTG CCC TCA ATT GTA ATT CTG GGT AAG ATT ATT TTA TTC CTT CCA TGT					
---	---	---	---	---	---
L V L P S I V I L G K I I L F L P C					
1683	1692	1701	1710	1719	1728
ATA AGC CGA AAG CTA AAA CGA ATT AAA AAA GGC TGG GAA AAG AGC CAA TTT CTG					
---	---	---	---	---	---
I S R K K L K R I K K G W E K S Q F L					

FIGURE 1F

1737	1746	1755	1764	1773	1782
GAA GAA GGT ATT GGA GGA ACA ATT CCT CAT GTC TCC CCG GAG AGG GTC ACA GTA					
E E G I G G T I P H V S P E R V T V					
1791	1800	1809	1818	1827	1836
ATG TGA TGA TAA ATG GTG TTC ACA GCT GCC ATA TAA AGT TCT ACT CAT GCC ATT					

M					
1845	1854	1863	1872	1881	1890
ATT TTT ATG ACT TCT ACG TTC AGT TAC AAG TAT GCT GTC AAA TTA TCG TGG GTT					
GA 3'					

FIGURE 1G

1	MES	I	S	M	G	S	P	K	S	L	S	E	T	C	L	P	N	G	I	N	G	I	K	D	A	R	K	7492448				
1	MES	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	K	g6572948				
31	V	T	V	G	V	I	G	S	G	D	F	A	K	S	L	T	I	R	L	I	R	C	G	Y	H	V	I	G	S	7492448		
6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g6572948			
61	R	N	P	K	F	A	S	E	F	F	P	H	V	V	D	V	T	H	H	E	D	A	L	T	K	T	N	I	I	F	7492448	
6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g6572948		
91	V	A	I	H	R	E	H	Y	T	S	L	W	D	L	R	H	L	L	V	G	K	I	L	I	D	V	S	N	N	M	7492448	
13	-	-	-	-	-	-	-	-	-	-	L	W	K	M	K	P	-	-	-	-	-	-	-	-	-	-	R	R	N	L	g6572948	
121	R	I	N	Q	Y	P	E	S	N	A	E	Y	L	A	S	L	F	P	D	S	L	I	V	K	G	F	N	V	V	S	7492448	
23	E	E	D	D	Y	L	H	K	D	T	G	-	E	T	S	M	L	K	R	P	V	L	-	-	-	-	-	-	-	-	g6572948	
151	A	W	A	L	Q	L	G	P	K	D	A	S	R	Q	V	Y	I	C	S	N	N	I	Q	A	R	Q	Q	V	I	E	7492448	
44	-	-	-	L	H	L	-	H	Q	T	A	H	A	D	E	F	D	C	P	S	E	L	Q	H	T	Q	E	-	-	-	g6572948	
181	L	A	R	Q	L	N	F	I	P	I	D	L	G	S	L	S	S	A	R	E	I	E	N	L	P	L	R	L	F	T	7492448	
67	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	F	P	g6572948
211	L	W	R	G	P	V	V	V	A	I	S	L	A	T	F	F	F	L	Y	S	F	V	R	D	V	I	H	P	Y	A	7492448	
70	Q	W	H	L	P	I	K	I	A	A	I	A	S	L	T	F	L	Y	T	L	L	R	E	V	I	H	P	L	A	g6572948		

FIGURE 2A

241 R N Q Q S D F Y K I P I E I V N K T L P I V A I T L L S L V 7492448
100 T S H Q Q Y F Y K I P I L V I N K V L P M V S I T L L A L V g6572948

271 Y L A G L L A A Y Q L Y Y G T K Y R R F P P W L E T W L Q 7492448
130 Y L P G V I A A I V Q L H N G T K Y K K F P H W L D K W M L g6572948

301 C R K Q L G L L S F F A M V H V A Y S L C L P M R R S E R 7492448
160 T R K Q F G L L S F F A V L H A I Y S L S Y P M R R S Y R g6572948

331 Y L F L N M A Y Q Q V H A N I E N S W N E E E V W R I E M Y 7492448
190 Y K L L N W A Y Q Q V Q Q N K E D A W I E H D V W R M E I Y g6572948

361 I S F G I M S L G L L S L L A V T S I P S V S N A L N W R E 7492448
220 V S L G I V G L A I L A L L A V T S I P S V S D S L T W R E g6572948

391 F S F I Q S T L G Y V A L L I S T F H V L I Y G W K R A F E 7492448
250 F H Y I Q S K L G I V S L L L G T I H A L I F A W N K W I D g6572948

421 E E Y Y R F Y T P P N F V L A L V L P S I V I L G K I I L F 7492448
280 I K Q F V W Y T P P T F M I A V F L P I V V L I F K S I L F g6572948

FIGURE 2B

Figure 2C

451	L	P	C	I	S	R	K	L	K	R	I	K	K	G	W	E	K	S	Q	F	L	E	G	I	G	T	I	P	7492448	
310	L	P	C	L	R	K	K	I	L	K	I	R	H	G	W	E	D	-	-	-	-	-	-	-	-	-	-	V	T	g6572948
481	H	V	S	P	E	R	V	-	T	V	M																		7492448	
329	K	I	N	K	T	E	I	C	S	Q	L																		g6572948	

FIGURE 2C